STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
 U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street.
 Alexandria, VA 22314

Revised 01/24/05

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER 9914	1/
ATTN: NEW RULES C	ASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTIVE	
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-	The submitted file was not saved in ASCII(DOS) lext, as required by the Sequence Rules. Please	
SVariable Length	Samuel of the state of the ASCII lead.	
	Sequence(s) contain n's or Xaa's representing more than one visidue. Per Sequence Rules, residue having variable terresent a single residue. Please present the marians and residue.	
	each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220> <223> section that some	-
· GPatentin 2.0	residue having variable length and indicate in the <220>-<223> section that some may be missing A "bug" in Patentin version 2.0.	
"bug"	A "bug" in Patentin version 2.0 has caused the <220>-<22)> section to be missing from animo acid previously coded nucleic seid and animo acid	
	sequences(s) Normally, Patentla would automatically generate this section from the the subsequent amino acides. Please manually copy the relevant \$2200.	
	previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to Artificial or Unknown recovered to the manually copy the relevant <220>-<223> section to Artificial or Unknown recovered to the manual ory <220>-<223> section to	
	the subsequent amino acid sequence. Please manually copy the relevant <220>-<223> section to Artificial or Unknown sequences.	
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(OLD RULES)		
	(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown) (3) SEQUENCE CHARACTERISTICS (Do not insert service)	
•	(A) SEQUENCE DESCRIPTION (Do not insert any sublications	
	(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 Skipped See	Please also adjust the "(ii) NUMBER OF SEQUENCES response to include the stapped sequences. Sequence(s)	
8 Skipped Sequences (NEW RULES)	Sequence(s) missing If intentional please insent the following lines for each skipped sequence: <100 sequence id number <400 sequence id number	
	\$4005 sequence id number	-
	<400> sequence id number	
9 Use of n's or Xaa's	•	
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	cer 1 823 of Sequence Rules, use of <220> <221> is MANDATORY if n's or Xaa's are present 1 < 220> to <223> section, please explain location of n or Xaa and which you do not see the present	
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	can only represent a single nucleotide: "Xaa" can only represent a single amino acid	
	AMC D: Financial Scill	

AMC - Biotechnology Systems Branch - 09/09/2003



1600

RAW SEQUENCE LISTING

DATE: 03/03/2005

PATENT APPLICATION: US/09/914,455B

TIME: 15:22:17

Input Set : A:\PTO.ST.txt

Output Set: N:\CRF4\03032005\I914455B.raw

3 <110> APPLICANT: Rosilio, Charles 5 <120> TITLE OF INVENTION: Method for Producing a Template of Sequences of Chemical or Biological Molecules for a Chemical or biological Analysis Device 8 <130> FILE REFERENCE: MM4464 10 <140> CURRENT APPLICATION NUMBER: US 09/914,455B C--> 11 <141> CURRENT FILING DATE: 2001-08-27 Does Not Comply 13 <150> PRIOR APPLICATION NUMBER: PCT/FR00/00550 Corrected Diskette Needed 14 <151> PRIOR FILING DATE: 1999-03-08 16 <160> NUMBER OF SEQ ID NOS: 3 18 <170> SOFTWARE: PatentIn version 3.1 20 <210> SEQ ID NO: 1 21 <211> LENGTH: 15 22 <212> TYPE: DNA 23 <213> ORGANISM: Illustration purpose only 25 <400> SEQUENCE: 1 26 atctcactca aataq 29 <210> SEO ID NO: 2 30 <211> LENGTH: 15 31 <212> TYPE: DNA 32 <213> ORGANISM: [Illustration purpose only 34 <400> SEQUENCE: 2 35 atctcaccca aatag 38 <210> SEQ ID NO: 3 39 <211> LENGTH: 19 40 <212> TYPE: DNA 41 <213> ORGANISM: (Illustration purpose only) INVAI 43 <400> SEQUENCE: 3 44 catagagtgg gtttatcca Mandatory
(2137 response has to be
either Artificial Unknown
or Genus Species.

VERIFICATION SUMMARY

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DATE: 03/03/2005

PATENT APPLICATION: US/09/914,455B

TIME: 15:22:18

Input Set : A:\PTO.ST.txt

Output Set: N:\CRF4\03032005\I914455B.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date